

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Lester, Henry A., et al.

(ii) TITLE OF INVENTION: DNA ENCODING INWARD RECTIFIER, G-PROTEIN
ACTIVATED, MAMMALIAN, POTASSIUM KGA CHANNEL

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Cooper & Dunham
- (B) STREET: 30 Rockefeller Plaza
- (C) CITY: New York
- (D) STATE: New York
- (E) COUNTRY: USA
- (F) ZIP: 10112

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US Not Yet Known
- (B) FILING DATE:
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: White, John P.
- (B) REGISTRATION NUMBER: 28,678
- (C) REFERENCE/DOCKET NUMBER: 43717/JPW/TEP

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 977-9550
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- (C) TELEX: 422523 COOP UI

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 32..1534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA	52
Met Ser Ala Leu Arg Arg Lys	
1 5	
TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC	100
Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly	
10 15 20	
TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC	148
Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro	
25 30 35	
AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG	196
Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val	
40 45 50 55	
CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC	244
Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu	
60 65 70	
TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC	292
Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe	
75 80 85	

ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG	340
Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp	
90 95 100	
GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC	388
Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn	
105 110 115	
TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT	436
Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu	
120 125 130 135	
TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC	484
Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile	
140 145 150	
ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC	532
Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile	
155 160 165	
CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG	580
Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys	
170 175 180	
ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT	628
Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His	
185 190 195	
GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG	676
Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val	
200 205 210 215	
GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG	724
Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys	
220 225 230	
CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC	772
Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp	
235 240 245	
CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT	820

Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe	
250 255 260	
CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC	868
Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro	
265 270 275	
TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG	916
Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val	
280 285 290 295	
GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA	964
Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln	
300 305 310	
GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT	1012
Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe	
315 320 325	
TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC	1060
Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser	
330 335 340	
CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA	1108
Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys	
345 350 355	
GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC	1156
Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala	
360 365 370 375	
ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA	1204
Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly	
380 385 390	
CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG	1252
Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr	
395 400 405	
GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT	1300
Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr	

410	415	420	
TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA			1348
Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg			
425	430	435	
ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC			1396
Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr			
440	445	450	455
ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA			1444
Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro			
460	465	470	
CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT			1492
Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn			
475	480	485	
CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA			1534
Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr			
490	495	500	
TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTGTAGT CCAATATTTG			1594
GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT			1654
CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA			1714
TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT			1774
TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA			1834
AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTCTA ATATATGTAT			1894
TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATACATACA			1954
TACATGCATA TGCACAGACA CATAACACA CATACTCATA TATATAAAAC ATACCCATAC			2014
AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAA AAAAAAAAAA AAAAAACTCG			2074
AG			2076

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ala Leu Arg Arg Lys Phe Gly Asp Asp Tyr Gln Val Val Thr
1 5 10 15

Thr Ser Ser Ser Gly Ser Gly Leu Gln Pro Gln Gly Pro Gly Gln Gly
20 25 30

Pro Gln Gln Gln Leu Val Pro Lys Lys Lys Arg Gln Arg Phe Val Asp
35 40 45

Lys Asn Gly Arg Cys Asn Val Gln His Gly Asn Leu Gly Ser Glu Thr
50 55 60

Ser Arg Tyr Leu Ser Asp Leu Phe Thr Thr Leu Val Asp Leu Lys Trp
65 70 75 80

Arg Trp Asn Leu Phe Ile Phe Ile Leu Thr Tyr Thr Val Ala Trp Leu
85 90 95

Phe Met Ala Ser Met Trp Trp Val Ile Ala Tyr Thr Arg Gly Asp Leu
100 105 110

Asn Lys Ala His Val Gly Asn Tyr Thr Pro Cys Val Ala Asn Val Tyr
115 120 125

Asn Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile
130 135 140

Gly Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile
145 150 155 160

Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu
165 170 175

Ile Gly Cys Met Phe Ile Lys Met Ser Gln Pro Lys Lys Arg Ala Glu
180 185 190

Thr Leu Met Phe Ser Glu His Ala Val Ile Ser Met Arg Asp Gly Lys
195 200 205

Leu Thr Leu Met Phe Arg Val Gly Asn Leu Arg Asn Ser His Met Val
210 215 220

Ser Ala Gln Ile Arg Cys Lys Leu Leu Lys Ser Arg Gln Thr Pro Glu
225 230 235 240

Gly Glu Phe Leu Pro Leu Asp Gln Leu Glu Leu Asp Val Gly Phe Ser
245 250 255

Thr Gly Ala Asp Gln Leu Phe Leu Val Ser Pro Leu Thr Ile Cys His
260 265 270

Val Ile Asp Ala Lys Ser Pro Phe Tyr Asp Leu Ser Gln Arg Ser Met
275 280 285

Gln Thr Glu Gln Phe Glu Val Val Val Ile Leu Glu Gly Ile Val Glu
290 295 300

Thr Thr Gly Met Thr Cys Gln Ala Arg Thr Ser Tyr Thr Glu Asp Glu
305 310 315 320

Val Leu Trp Gly His Arg Phe Phe Pro Val Ile Ser Leu Glu Glu Gly
325 330 335

Phe Phe Lys Val Asp Tyr Ser Gln Phe His Ala Thr Phe Glu Val Pro
340 345 350

Thr Pro Pro Tyr Ser Val Lys Glu Gln Glu Glu Met Leu Leu Met Ser
355 360 365

Ser Pro Leu Ile Ala Pro Ala Ile Thr Asn Ser Lys Glu Arg His Asn
370 375 380

Ser Asp Arg Phe Thr
500